COMPARING RESULTS OBTAINED FROM THE PATHWAY ACTIVITY PROFILING (PAPI) ALGORITHM WITH 13C-BASED METABOLIC FLUX ANALYSIS.

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Metabolomics has gained increased popularity in the last 10 years. This popularity comes from its use as a functional genomics tool and its diverse range of potential applications. However, metabolomics data sets are usually complex, difficult to interpret and challenging to correlate. The Pathway Activity Profiling (PAPi) (1) is a method developed in our group to correlate metabolite levels with potential metabolic pathways likely to be active inside the cells. This method uses the number of metabolites detected from each metabolic pathway and their relative abundances in the samples to predict the activity of different pathways. PAPi has been recently published and became very popular. However, PAPi consider that pathways which intermediate are found at lower intracellular levels are down-regulated compared to pathways with intermediates accumulating inside the cells. This assumption has been controversial, and, therefore, we propose to compare the results generated by PAPi with metabolic flux analysis of two different microorganisms: *Escherichia coli* and *Enterococcus faecalis*. Based in the fraction of ^{13}C-labelling distribution in the biomass, we estimated the flux through different metabolic pathways from the central carbon metabolism of these bacteria when growing under different environmental conditions. Metabolic flux analysis is the ultimate measurement of metabolic pathway activity, and should answer the question of whether or not the intracellular metabolic intermediates of a pathway accumulate when down-regulated.

(1) Aggio, R., Ruggiero, K. and Villas-Boas, S. (2010) Pathway Activity Profiling (PAPi): from metabolite profile to the metabolic pathway activity. Bioinformatics. doi:10.1093/bioinformatics/btq567.